

O'Bryen, Barbara

From: Swope, Sheridan
Sent: Wednesday, August 11, 2004 2:02 PM
To: O'Bryen, Barbara
Subject: 09/712,338

Barb, Would you do me the favor of doing the following alignment?

SID 2 of 09/712,338 with NCBI Acc#S38953 (<http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?db=protein&val=481619>)
Thanks!

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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:27:53 ; Search time 0.001 seconds
(without alignments)
234.785 Million cell updates/sec

Title: US-09-712-338-2

Perfect score: 2979

Sequence: 1 MEGYFLSLVPLVAASWALP.....HTOSSVPLTATSMSSVGMVA 555

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1 seqs, 423 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : s38953.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	894	30.0	423	1	s38953

TOIG of: s38953

ALIGNMENTS

RESULT 1

s38953

; TOIG of: s38953 check: 3675 from: 1 to: 423

; P1:S38953 - carboxypeptidase D (EC 3.4.16.6) - Penicillium janthinellum
; N/Alternate names: carboxypeptidase S1
; C/Species: Penicillium janthinellum
; C/Date: 18-Feb-1994 #sequence_revision 19-Apr-1996 #text_change 31-Mar-2000
; C/Accession: S38953
; R/Svendsen, I.; Hofmann, T.; Endrizzi, J.; Remington, S.J.; Breddam, K.
; FEBS Lett. 333, 39-43, 1993
; A/Title: The primary structure of carboxypeptidase S1 from Penicillium
; janthinellum.
; A/Reference number: S38953; MUID:94039747; PMID:8224168
; A/Accession: S38953
; A/Status: preliminary
; A/Molecule type: protein
; A/Residues: 1-423 <SVE>
; C/Superfamily: serine carboxypeptidase
; C/Keywords: hydrolase; serine carboxypeptidase
; S38953 Length: 423 August 11, 2004 14:21 Type: P Check: 3675 ..
s38953

Query Match 30.0%; Score 894; DB 1; Length 423;

Best local Similarity 40.1%; Pred. No. 0;

Matches 186; Conservative 66; Mismatches 160; Indels 52; Gaps 8;

QY 59 GYCETTRGVKSYSGYVDTPSPSHTFWFFEFARBNPETAPITLWLNCGPGSDSLIGLPEEL 118
Db 6 GICETTPGVNQYSGYLSVGSNNMWFNFPEARNPQAPLAANFNGPGSCSSWIGLQEN 65
QY 119 GPCH-VNSTFDDYINPHSWNEVSNLLFSLQPLGVGFYSYDVGSIINPVITGVVENSFAG 177
Db 66 GPCHEVNGDSTPISLNSNNYANNMIXIDQPIGVGFSGV----- 104
QY 178 VQGRYPTIDATLIDTNNLAEEAWEILQGLSLGSLDSRVQSKDFSLWTESYGGHYGPA 237
Db 105 -----TDDVT---STVTAAPYVWNLQAFYAQRPEYESR-----DPAIFTESYGGHYGPE 151
QY 238 FPNHFEQNERIANGSVNGVOLNFNSLGIINGIIIDEAIAQAPYYPPEFVAVNNTYGIKAVNET 297
Db 152 FASYIEQQNAALKAGSVTGQNVNIVALGVNNGWIDSTIQEKAYIDFSYNNSYQOIIDSST 211
QY 298 VYNYMKFANQMPNGCODLISTCKQTNRTALADYALCAEATNMCRDNVEGYPYAPAGRGVY 357
Db 212 RSLLDAYN---NQLPALQCSQSGST-----SDCTNADSVCYQNIETGPISSGGDFDY 263
QY 358 DIRHPYDDPTPFSSYNNKFLAKDSVMDAIGVNNINTQSNNDVYAFQQTGDFVWFNFIEDL 417
Db 264 DIREPSNDPYPKTYSTYLSDPVVKAIGARTNYQECNPGPNKFASTGDNP-RSFLSTL 322
QY 418 EELIALPVRSVLSLYGDADYICNWFGQAVSLAANYSAQAQPSAGYTPLKVNGVYGEYR 477
Db 323 SSVVQSGINVLWAGDADWICNWLGNVEVANAVDPGNAQPSALDLAPYTVNGVERGQFK 382
QY 478 EYGNFSFTRVYEAGHEVYQFIASLQLFNRTIFGWDIAEQKK 521
Db 383 TVDNFSFLKVGAGHEVYQFDALQAFKQII-----QKK 418

Search completed: August 11, 2004, 14:27:53

Job time : 0.001 secs